

SEQUENCE LISTING

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 Chan, Sham-Yuen
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<120> Expression System for Factor VIII

<130> MSB-7255.1

<140>

<141>

<160> 2

<170> PatentIn Ver. 2.0

<210> 1

<211> 1438

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Derived from
 human factor VIII sequence

<400> 1

Ala	Thr	Arg	Arg	Tyr	Tyr	Leu	Gly	Ala	Val	Glu	Leu	Ser	Trp	Asp	Tyr
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Met	Gln	Ser	Asp	Leu	Gly	Glu	Leu	Pro	Val	Asp	Ala	Arg	Phe	Pro	Pro
			20					25					30		

Arg	Val	Pro	Lys	Ser	Phe	Pro	Phe	Asn	Thr	Ser	Val	Val	Tyr	Lys	Lys
		35					40					45			

Thr	Leu	Phe	Val	Glu	Phe	Thr	Val	His	Leu	Phe	Asn	Ile	Ala	Lys	Pro
	50					55					60				

Arg	Pro	Pro	Trp	Met	Gly	Leu	Leu	Gly	Pro	Thr	Ile	Gln	Ala	Glu	Val
65					70					75					80

Tyr	Asp	Thr	Val	Val	Ile	Thr	Leu	Lys	Asn	Met	Ala	Ser	His	Pro	Val
				85					90					95	

Ser	Leu	His	Ala	Val	Gly	Val	Ser	Tyr	Trp	Lys	Ala	Ser	Glu	Gly	Ala
			100					105					110		

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Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe
      565                                570                                575

Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln
      580                                585                                590

Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe
      595                                600                                605

Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser
      610                                615                                620

Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
      625                                630                                635                                640

Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr
      645                                650                                655

Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro
      660                                665                                670

Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp
      675                                680                                685

Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala
      690                                695                                700

Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu
      705                                710                                715                                720

Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala
      725                                730                                735

Ile Glu Pro Arg Ser Phe Ser Gln Asn Pro Pro Val Leu Lys Arg His
      740                                745                                750

Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile
      755                                760                                765

Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp
      770                                775                                780

Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys
      785                                790                                795                                800

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Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly
 805 810 815
 Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser
 820 825 830
 Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser
 835 840 845
 Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu
 850 855 860
 Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr
 865 870 875 880
 Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile
 885 890 895
 Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe
 900 905 910
 Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His
 915 920 925
 Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe
 930 935 940
 Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro
 945 950 955 960
 Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln
 965 970 975
 Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr
 980 985 990
 Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro
 995 1000 1005
 Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe
 1010 1015 1020
 His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met

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1025              1030              1035              1040
Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser Asn
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Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg
      1060              1065              1070
Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val
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Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val
      1090              1095              1100
Glu Cys Leu Ile Gly Glu His Leu His Ala Gly Met Ser Thr Leu Phe
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Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser Gly
      1125              1130              1135
His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp
      1140              1145              1150
Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp
      1155              1160              1165
Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro
      1170              1175              1180
Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser
1185              1190              1195              1200
Ser Leu Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys
      1205              1210              1215
Lys Trp Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe
      1220              1225              1230
Phe Gly Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro
      1235              1240              1245
Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile
      1250              1255              1260

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Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys
1265 1270 1275 1280

Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile
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Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser
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Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln
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Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met
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Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Ser
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Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His Gln
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Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn
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Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu Leu
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Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala
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Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr
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<210> 2

<211> 402

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Derived from
Epstein-Barr virus sequence

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120
ggccccccag gaaagacccc cgggggggcat cgggggggtg ttggcgggtc atgggggggg
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cgggtcatgc cgcgcattcc tggaaaaagt ggagggggcg tggccttccc cccgcggccc
240
cctagcccc cgcagagag cggcgcaacg gcgggcgagc ggcggggggt cggggtccgc
300
gggctccggg ggctgcgggc ggtggatggc ggctggcggt ccgggggatcg ggggggggtc
360
ggggggcgct gcgcgggcgc agccatgcgt gaccgtgatg ag
402